Supporting Online Summary Tables for

Aging Enhances Production of Reactive Oxygen Species and Bactericidal Activity in Peritoneal Macrophages by Up-Regulating Classical Activation Pathways

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Table S1: Age-Dependent Protein Abundance Changes in Peritoneal Macrophages (77 proteins)[1]

I. Resting Conditions (No LPS Stimulation) (23 proteins)

A. Down-regulated (11 proteins)

1. Cytoskeletal/Motility (2 proteins)
   - i. actin* (Actc1)(id 11459, 11461, 11464, 11465, 11475)(-6.1 ± 0.4) – Major cytoskeletal protein that mediate motility, which includes α/β cytosolic actins that polymerize to form structural filaments as well as ϒ-actin isoform that regulates rapid induction of actin nucleation to promote α/β actin polymer formation.
   - ii. chaperonin containing Tcp1, subunit 3 (gamma) (Cct3) (id 12462) (-6.0 ± 0.5) – Essential ATP-dependent complex required in maturation of cytoskeletal proteins actin and tubulin (*1*).
2. Phagocytosis and Signaling (0 proteins)
3. Antigen Processing/Differentiation (2 proteins)
   - i. melanoma antigen (Mela) (id 17276) (-6.6 ± 0.7) – Antigenic determinant expressed on many tumor cells (*2*).
   - ii. heat shock protein 1B** (Hsp70-1B)(id 15511) (-1.7 ± 0.2) – Blocks apoptosis through inhibition of caspases.
4. Macrophage Activation, Cytokine Production, Oxidative Stress Response, and Apoptosis (3 proteins)
   - i. arginase I (id 11846) (-13.1 ± 0.8) – Depletes arginine to inhibit NO generation by NOS; part of alternative activation pathway in macrophages that contributes to suppression of T-cell response. Insufficient arginine can uncouple NOS to enhance generation of superoxide (*3-6*). arginase activity plays a critical role to induce an district alternative activation program (M2 phenotype) to that involving classical activation(*7*).
   - ii. AHNAK nucleoprotein* (desmoyokin) (id 66395) (-9.4 ± 0.8) – Potentiates PKC-dependent signaling (*8*); essential role in T-cell signaling.
   - iii. glutathione S-transferase, pi 1 (Gstp1) (id 14870) (-7.7 ± 0.7) – Catalyzes reversible protein S-glutathionylation to regulate diverse range of intracellular pathways in response to oxidative stress (*9-10*).
5. Antimicrobial Activity (1 protein)
   - i. histone cluster 1**, H2ba (id 319177) (-9 ± 1) – DNA binding protein that associates with nucleosome and whose abundance is associated with antimicrobial activity.
6. Other (3 proteins)
   - i. Euk. translation initiation factor 3** (id 78655) (-8.2 ± 0.9) – Promotes protein biosynthesis.
   - ii. SET translocation (Set) (id 56086) (-5.6 ± 0.6) – DNA binding protein associated with nucleosome assembly.
   - iii. cDNA sequence BC085271 (id 434632) (-5.6 ± 0.5) – Hypothetical protein related to Set with similarity to protein phosphatase 2A inhibitor.

B. Up-regulated (12 proteins)

1. Cytoskeletal/Motility (1 protein)
   - i. myosin If* (myo1F) (id 17916) (6.2 ± 0.6) - Nonmuscle myosin associated with calcium-dependent cell motility through calmodulin binding.
2. Phagocytosis and Signaling (2 proteins)
   - i. arginyl-tRNA synthase** (Rars)(id 104458) (3.9 ± 0.5) – Associates with p43 in aminoacyl-tRNA synthetase complex, where secreted p43 regulates local inflammatory response and macrophage chemotaxis.
   - ii. dihydropyrimidinase-like 2 (Dpysl1) (id 12934) (3.5 ± 0.4) – Associated with lymphocyte transendothelial migration, cell differentiation, and proliferation.
3. Antigen Processing/Differentiation (4 proteins)
   - i. kinesin light chain (id 16594) (10.6 ± 0.7) – Microtubule motor activity, links to bacterial localization in vacuole following infection.
   - ii. phophoinositide-3-kinase adaptor protein 1 (Pik3ap1 or BCAP) (id 83490) (9.5 ± 0.9) – Mediates downstream signaling from antigen receptors to promote activation of NFκB(*11*).

iii. HECT, UBA and WWE domain containg 1 (Huwe1) (id 59026) (7.2 ± 0.6) – E3 ubiquitin ligase that mediates targeted proteasomal degradation.

iv. tripeptidyl peptidase (Tpp1) (id 12751) (5.3 ± 0.4) – Serine-type peptidase that degrades lysosomal exopeptides from N-terminus.

4. Macrophage Activation, Cytokine Production, Oxidative Stress Response, and Apoptosis (1 protein)

i. nicotinamide phosphoribosyltransferase (NaPRT or Nampt) (id 59027) (10.5 ± 0.9) – Enhances cell survival pathways through blockage of macrophage apoptosis induced by ER stressor via IL-6 induction and downstream activation of STAT3 (*12*). Mediates NAD synthesis through rescue pathways, where NaPRT catalyzes formation of nicotinamide mononucleotide (NMN) that, in turn, reduces NAD and ATP depletion in cells undergoing PARP-1 hyperactivation to delay cell death (*13*). Consistent with diminished ability of macrophages from aged mice to express and activate STAT1 (*14*).

5. Antimicrobial Activity (0 proteins)

6. Other (4 proteins)

i. phosphoribosyl pyrophosphate amidotransferase (Ppat) (id 231327) (10.8 ± 0.5) – Key enzyme involved in glutamate and purine metabolism.

ii. splicing factor 3b, subunit 2 (Sf3b2) (id 319322) (6.5 ± 0.2) – Interacts with Smad to mediate transcriptional regulation in response to TGF (*15*).

iii. methionine tRNA synthetase (Mars) (id 216443) (6.4 ± 0.8) – Translational control of protein synthesis.

iv. phosphoglycerate mutase (Pgam2) (id 56012) (2.4 ± 0.3) – Glycolytic enzyme upregulated by glucocorticoids in neutrophils as part of stress response that has previously identified as target of anti-inflammatory isoxazole derivative leflunomide (HWA 486) in macrophages (*16*).

II. LPS Stimulation (54 proteins)

A. Down-regulated (6 proteins)

1. Cytoskeletal/Motility (0 proteins)

2. Phagocytosis and Signaling (0 proteins)

3. Antigen Processing/Differentiation (0 proteins)

4. Macrophage Activation, Cytokine Production, Oxidative Stress Response, and Apoptosis (3 proteins)

i. ADP/ATP exchanger** (Slc25a5) (id 11740) (-3.2 ± 0.7) – Linked to apoptosis through formation of permeability pore.

ii. 26S subunit of proteasome** (Psmd3) (id 22123) (-3.0 ± 0.6) – Central role in ATP-dependent protein degradation, including NFkB activation.

iii. E2Q ubiquitin conjugating enzyme* (Ube2q1) (id 70093) (-2.8 ± 0.1) – Directed protein degradation through proteasome.

5. Antimicrobial Activity (0 proteins)

6. Other (3 proteins)

i. hemoglobin* (id 15129) (-5.4 ± 0.5) – During inflammation macrophages engulf oxidized erythrocytes in a process associated with cytokine release (*17*).

ii. keratin 28* (Krt28) (id 70843) (-3.0 ± 0.3) – Consistent with infiltration of macrophages into skin as part of inflammatory response (*18*).

iii. elongation factor 2* (Eef2) (id 13629) (-1.8 ± 0.3) – Translation elongation factor known to be critical to immune function response.

B. Up-regulated (48 proteins)

1. Cytoskeletal/Motility (9 proteins)

i. γ-actin (Actg1) (id 11465) (3.1 ± 0.3) – Cytosolic γ-actin regulates rapid induction of actin nucleation to upregulate actin polymerization.

ii. S100** (id 20198) (3.1 ± 0.3) – Calcium binding protein that binds p53 to modulate cell motility.

iii. coactosin (id 72042) (2.1 ± 0.5) – Actin binding protein with known role in promoting antimicrobial defense response against fungi.

iv. arginyl-tRNA synthetase* (id 104458) (2.1 ± 0.2) – Links to p43, which promotes macrophage chemotaxis following its secretion.

v. filamin gamma (FlnC) (id 68794) (1.9 ± 0.5) – Anchors actin filaments to the membrane.

vi. macrophage capping protein (CapG)(id 12332) (1.5 ± 0.1) – Required for motility, and critical to resist infection by Listeria; related to gelasin/villin capping proteins.

vii. tubulin, alpha 1A* (Tuba1a) (id 22142) (1.5 ± 0.1) – Contributes to microtubule based motility.

viii. enolase* (id 13806) (1.4 ± 0.2) – Glycolytic enzyme with dual role that binds plasminogen to mediate LPS-dependent motility (*19*).

ix. α1-actin* (Acta1) (id 11459) (1.3 ± 0.3) – Cytosolic actin, major cytoskeletal protein that forms structural filaments.

2. Phagocytosis and Signaling (6 proteins)
   i. transgelin 2 (id 21346) (2.0 ± 0.2) – 22kDa actin-binding regulatory protein within calponin family that stabilizes actin filaments to prevent formation of podosomes associated with invasive malignant motility (*20*). Transgelin 2 is associated with suppression of MMP-9, which is highly expressed in cells at sites of inflammation in response to TNFα-dependent pathways. Contains EF-hand calcium binding sites as well as interaction sites for caseine kinase II and PKC (*20*). Observed to be upregulated in RAW 264.7 macrophages following *Salmonella* infection (*21*).
   ii. tyrosine 3-monooxygenase (Ywhaz) (id 22631) (1.8 ± 0.3) – Cell cycle/signaling, part of 14-3-3 family that binds to phosphoserine and is linked to MAPK-dependent inflammatory pathways.
   iii. coronin (id 12721) (1.8 ± 0.3) – Actin binding protein critical for chemokine mediated migration that plays key role in phago-lysosomal fusion. Coronin is required for an early step in phagosome formation that is consistent with a role in modulating actin polymerization (*22*).
   iv. adenylate cyclase-associated protein 1 (Cap1) (id 12331) (1.8 ± 0.3) – Actin binding protein associated with inflammatory responses to induce ameboidal cell migration and receptor mediated endocytosis.
   v. annexin A5** (Anxa5) (id 11747) (1.7 ± 0.2) – Voltage-dependent calcium channel linked to immune reaction; Knock-outs result in down-regulation of inflammatory response.
   vi. moesin* (membrane-organizing extension spike protein) (id 17698) (1.0 ± 0.2) – Regulation of actin cytoskeleton, links to TNFα production.

3. Antigen Processing/Differentiation (4 proteins)
   i. filamin alpha (FlnA) (id 192176) (1.7 ± 0.1) – Calmodulin-dependent actin binding protein critical to initiating actin polymerization and cytoskeleton anchorage at the membrane, where FlnA acts to recruit signal transduction complexes that activate the MAPK pathway and ERK phosphorylation (*23-26*).
   ii. cathepsin D (Ctsd) (id 13033) (1.4 ± 0.3) – Endopeptidase in lysosome linked to resolution of inflammation through activation of caspase 8 to promote apoptosis (*27*)
   iii. histocompatibility 2, D-region (H2-D1) (id 14964) (1.3 ± 0.3) – H-2D surface glycoprotein linked to antigen processing/presentation via MHC class I immune response.
   iv. heat shock protein 8* (Hsc70) (id 15481) (1.2 ± 0.1) – Involvement in protein transport in the endoplasmic reticulum critical for antigen presentation, as well as down-regulation of cytokine production through ubiquitin-proteasome pathway (*28-31*).

4. Macrophage Activation, Cytokine Production, Oxidative Stress Response, and Apoptosis (21 proteins)
   i. TNFα inhibitory protein (TIP-B1) or SH3 domain binding glutamic acid rich protein (Sh3bgrl3) (id 73723) (4.4 ± 0.4) - Function of intact protein is uncertain, but post-translational modification of C-terminus sequence protects cells from lysis induced by TNFα.
   ii. esterase D/formylglutathione hydrolase** (FGH) (id 13885) (4.2 ± 0.2) – Antioxidant protein that catalyzes hydrolysis of S-formylglutathione to glutathione + formate.
   iii. Gm2a (GM2 ganglioside activator protein) (id 14667) (3.9 ± 0.5) – Glycosphingo lipid transporter, blocks phospholipase D activity; oxidized LDL elevates this protein in monocyte-derived macrophages.
   iv. annexin A4 (id 11746) (3.9 ± 0.4) – Colocalizes with phagosomes and exerts antibacterial function through suppression of *S. aureus* attachment to macrophages.
   v. glutathione peroxidase (Gpx1) (id 14775) (2.9 ± 0.4) – Antioxidant protein that uses glutathione to catalyze the reduction of peroxides.
   vi. annexin A6 (Anxa6) (id 11749) (2.7 ± 0.2) – Anxa6 mobilization form cholesterol rich lipid rafts orchestrates macrophage reprogramming in response to oxidative stress to mediate increases in calcium signaling and upregulation of respiratory burst through activation of calmodulin-dependent pathways (e.g., CaM-KII)(*32-33*). Anxa6 recruits GTPase activating proteins (e.g., p120GAP) to plasma membrane to inactivate Ras (*34*). Anxa6 is elevated during obesity as part of global inflammatory response (*35-36*).
   vii. arachidonate-5-lipoxygenase activating protein (id 11690) (2.3 ± 0.2) – Downstream of Toll-receptors; key to formation of leukotrienes, linked to inflammatory response; activity increases during senescence via p53/p21 pathways.

viii. cathepsin B (Ctsb) (id 13030) (2.3 ± 0.2) – Cysteine protease in lysosomes involved in antigen degradation that plays an active role in inflammatory process through mediation of TNFα containing vesicle trafficking to plasma membrane (*37*). Associated with antigen presentation/degradation.

ix. peroxiredoxin* (Prx) (id 54683) (2.1 ± 0.3) – Antioxidant protein that increases in abundance in response to oxidative stress to limit oxidative damage and prevent cell death (anti-apoptotic) (*38-39*).

x. malate dehydrogenase* (Mdh2) (id 17448) (2.0 ± 0.3) – Important for moving reducing equivalents (NADH) across mitochondrial membrane, coupled to antioxidant response and metabolism.

xi. annexin A2* (Anxa2) (id 12306) (2.0 ± 0.2) – soluble mediator of macrophage activation through Tyr-kinase activity and calcium-dependent pathways.

xii. ubiquitin-like modifier activating enzyme (Uba1) (id 22201) (2.0 ± 0.2) – Role in preventing cell damage, stress response, and proteolysis.

xiii. phosphoglycerate kinase (PGK) (id 18655) (1.9 ± 0.3) – Overexpression reduces cyclooxygenase-2 (COX-2) to diminish inflammatory response.

xiv. lymphocyte cytosolic protein (Lcp1) (id 18826) (1.8 ± 0.2) – Actin binding protein that is critical to adhesion-dependent respiratory burst and secretion of IL1b in macrophages.

xv. cystatin B (id 13014) (1.8 ± 0.4) – Cysteine proteinases linked to cleavage of MARCKS protein in macrophages to promote calmodulin mobilization and $NO^{\bullet}$ production (*40*).

xvi. prolyl 4-hydroxylase** (id 18453) (1.7 ± 0.4) – Protein disulfide isomerase linked to stress response/aging; part of misfolded protein /oxidative stress response involving thioredoxin.

xvii. annexin A1 (id 16952) (1.5 ± 0.2) – Linked to protective role during inflammatory response (*41*) and upregulation of LPS-dependent iNOS pathway through the phoshorylation of ERK-1 and ERK-2 (*42*).

xviii. heat shock protein 90 alpha* (Hsp90ab1) (id 15516) (1.4 ± 0.2) – Critical role in type I and II interferon pathways; promote activation of proinflammatory transcription factors (*43*).

xix. aldehyde dehydrogenase** (ALDH-2) (id 11669) (1.4 ± 0.3) – Antioxidant protein in mitochondria linked to $NO^{\bullet}$ production in pathway that is distinct from NOS.

xx. heat shock protein 5 (GRP78 or Bip)(id 14828) (1.1 ± 0.3) – Part of stress response that promotes $NO^{\bullet}$ production and scavenger receptor mediated secretion of TNF-α (*44*) in macrophages. Part of ER stress response pathway that controls cell fate (apoptosis), and whose activity has been implicated in mediating aging response (*45*). Implicated in nonclassic antigen presentation (*46*) and regulation of cytotoxic T cell responses (*47*).

xxi. Gm2423 protein (id 100039786) (0.9 ± 0.1) – Similar to YWHAQ protein, which is a member of the 14-3-3 family of signaling proteins involved in apoptotic response.

5. Antimicrobial (4 proteins)

i. histidine ammonia lyase (Hal) (id 15109) (2.5 ± 0.1) – Histidine degradation and nitrogen metabolism, proposed antimicrobial function.

ii. ferritin light chain** (id 14325) (2.2 ± 0.1) – Chelates iron as part of antimicrobial function and upregulated within 4 hrs following LPS stimulation in response to $NO^{\bullet}$; commonly used to detect macrophage activation syndrome (*48*).

iii. lysozyme* (Lyz) (id 17105) (1.7 ± 0.3) – Secreted antimicrobial protein plays critical role in defense response against bacteria through cell wall degradation of Gram-positive bacteria.

iv. modifier of Min2** (Mom2) (id 11946) (1.1 ± 0.2) – Modifier locus linked to penetrance of mutations in tumor-suppressor genes that maps within exon 3 of the alpha subunit of ATP synthase (Atp5a1) (*49*). Mom2 is down-regulated following bacterial infection (*50*).

6. Other (4 proteins)

i. vesicle amine transport protein 1 homolog* (VAT-1) (id 26949) (4.0 ± 0.2) – Part of superfamily of medium-chain dehydrogenases and reductases with genetic locus near BRCA1(*51*). Upregulated in immune organs upon environmental exposures to biophenol A (*52*).

ii. ribosomal protein L4 (Rpl4) (id 67891) (2.6 ± 0.4) – Ribosomal protein, linked to enhanced rates of protein synthesis that is upregulated in cells in response to oxidative stress (*53*).

iii. pyruvate kinase** (id 18746) (1.2 ± 0.2) – Glycolytic enzyme that is up-regulated in response to MAPK kinase activation, which occurs during macrophage activation.
iv. EG666904 (id 666904) (1.6 ± 0.1) – No known function.

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[1] Each protein name is listed prior to i) an entrez gene identifier (http://www.ncbi.nlm.nih.gov/sites/entrez?db=pubmed), ii) age-dependent abundance change (log_2 scale), and iii) a description of function and relationship to immune function. Protein abundance changes were calculated from accurate mass and time tag (AMT) data using the RRollUp method in the quantitative analysis tool DAnTE (*54*), where the most abundant peptide across all data sets is used as a reference to calculate the ratios of protein abundances. Protein abundance is reported as the median of the resulting peptide abundances, where statistical significance is calculated from the ratio of the protein abundances using a cut-off at 5% FDR. 33 Proteins (* or **) were identified in Salmonella containing vesicles (*55*), where 14 (**) were observed only following infection in the *Salmonella* containing vesicles. These results emphasize that observed age-dependent changes in proteins are highly relevant to innate immunity and highlight the role of age-dependent changes in specific pathways associated with pathogen phagocytosis and killing. Additional proteins on list highlight role of macrophages in antigen processing and presentation as part of adaptive immune response.

Table S2: Overrepresented Annotations in Peritoneal Macrophage Protein Database Compared to the Combined Database for the Mouse Proteome

Annotation[a]	Term/Keyword	Genes[b]	Fold Enrichment[c]	Adjusted p-value[d]
GO Biological Process	Response to Stimulus	134	1.54	2.64E-04
	Defense to Response	58	2.04	3.80E-04
	Response to Biotic Stimulus	61	2.00	7.32E-04
	Response to Stress	90	1.64	1.83E-03
	Response to External Stimulus	37	2.17	3.28E-03
	Immune Response	51	1.91	3.86E-03
	Response to Other Organism	33	2.15	1.02E-02
	Chemotaxis	10	4.46	1.53E-02
	Response to Pathogen or Parasite	32	2.12	1.56E-02
	Response to Wounding	30	2.13	1.74E-02
	Response to Bacteria	6	7.41	2.05E-02
	Defense Response to Bacteria	5	8.77	3.09E-02
	Lymphocyte Proliferation	10	3.83	4.15E-02
GO Cellular Component	Vacuole	36	2.69	1.85E-05
	Lysosome	33	2.86	2.99E-05

[a]Annotation is derived from David Bioinformatics Resources to identify gene ontology (GO) terms and keywords, as described in Experimental Procedures. [b]Number of protein identifications matching genes encoded in specified process or cellular component. [c]Elevated abundances of identified proteins within each GO category relative to expectations based on entire pooled database of multiple mouse tissue samples, as described previously (*56*). [d]Overrepresented GO biological proecesses and cellular components were identified following determination of p values calculated using the Fisher exact test and a hypergeometric distribution, where adjusted p values are used to correct for multiplicity of testing using Benjamini-Hochberg adjustment method, assuming $p < 0.05$ is significant.

Table S3: Tandem Mass Spectrometric Identification of Proteasome Subunits[1]

Proteasome Subunits	Young		Old	
	NT	+ LPS	NT	+ LPS
I. Immunoproeasome				
28 subunit, alpha (PA28alpha)		+	+	+
28 subunit, beta (PA28beta)	+	+	+	+
subunit, beta type 9 (large multifunctional peptidase 2)(β1i)			+	+
subunit, beta type 10 (♄2i)	+	+	+	+
subunit, beta type 8 (large multifunctional peptidase 7) (β5i)				+
assembly chaperone 3				+
II. Lid of P700 Supramolecular Regulatory Protein Complex (Recognition of Ubiquitinated Proteins)				
26S subunit, non-ATPase, 2 (Rpn1)	+		+	+
26S subunit, non-ATPase, 1 (Rpn2)			+	+
26S subunit, non-ATPase, 3 (Rpn3)				+
26S subunit, non-ATPase, 12 (Rpn5)	+			+
26S subunit, non-ATPase, 11 (Rpn6)	+		+	+
26S subunit, non-ATPase, 6 (Rpn7)				+
26S subunit, non-ATPase, 7 (Rpn8)			+	+
26S subunit, non-ATPase, 4 (Rpn10)			+	+
26S subunit, non-ATPase, 5				+
26S subunit, non-ATPase, 14 (Rpn11)	+			+
III. Base of P700 Supramolecular Regulatory Protein Complex (Unfolds Proteins and Opens α-Ring)				
26S subunit, ATPase 2 (Rpt1)	+	+	+	+
26S subunit, ATPase 1 (Rpt2)		+	+	
26S subunit, ATPase, 4 (Rpt3)	+		+	+
26S subunit, ATPase, 6 (Rpt4)			+	+
26S subunit, ATPase 3 (Rpt5)	+	+	+	+
26S subunit, ATPase, 5 (Rpt6)		+	+	
IV. 20 S Core Protein Complex				
subunit, alpha type 6 (α1)	+		+	+
subunit, alpha type 2 (α2)	+	+	+	+
subunit, alpha type 4 (α3)			+	+
subunit, alpha type 7 (α4)	+		+	+
subunit, alpha type 5 (α5)	+		+	
subunit, alpha type 1 (α6)	+		+	+
subunit, alpha type 3 (α7)		+	+	+
subunit, alpha type, 8	+		+	+
subunit, beta type 6 (β1)	+	+	+	+

subunit, beta type 3 (β3)			+
subunit, beta type 2 (β4)		+	+
subunit, beta type 5 (β5)		+	+
subunit, beta type 1 (β6)		+	+
subunit, beta type 4 (β7)	+	+	+

[1]Correspondence between identified proteins and individual subnits within the proteasome proteins used the David Bioinformatics Resources (http://david.abcc.ncifcrf.gov/content.jsp?file=citation.htm) to identify proteins and subunit compositions of immunoproteasome, lid of P700 regultory complex, base of P700 regulatory complex, and 20S proteasome core (*57-58*).

Table S4: Tandem MS Identification of Central Proteins in MHC-I and MHC-II Antigen Presentation Pathways[1]

Antigen Processing Proteins	Young		Old	
	NT	+ LPS	NT	+ LPS
I. MHC-I Pathway				
proteasome (prosome, macropain) 28 subunit, alpha (PA28α)		+	+	+
proteasome (prosome, macropain) 28 subunit, beta (PA28β)	+	+	+	+
heat shock protein 5 (BiP)	+		+	+
calnexin (CANX)	+	+	+	+
protein disulfide isomerase associated 3 (BRp57)	+	+	+	+
calreticulin (CALR)	+	+	+	+
beta-2 microglobulin (β2m)	+	+	+	+
heat shock protein 8 (Hsp70)	+	+	+	+
heat shock protein 1-like (Hsp70)	+	+	+	+
heat shock protein 90 alpha (cytosolic), class B (Hsp90β)	+	+	+	+
heat shock protein 90, alpha (cytosolic), class A (Hsp90α)	+	+	+	+
heat shock protein 4 (Hsp70)	+	+	+	+
histocompatibility 2, D region locus 1 (MHCI)				+
TAP binding protein	+	+	+	
II. MHC-II Pathway				
legumain (AEP)	+	+	+	+
histocompatibility 2, class II antigen A, alpha (MHCII)	+	+		+
cathepsin B (CTSB)	+	+	+	+
cathepsin L (CTSL)		+	+	+
cathepsin S (CTSS)				+
histocompatibility 2, class II antigen A, beta 1	+	+		
histocompatibility 2, class II antigen E beta (MHCII)		+	+	+

[1]Correspondence between identified proteins and MHC-I and MHC-II antigen presentation pathways used the David Bioinformatics Resources (http://david.abcc.ncifcrf.gov/content.jsp?file=citation.htm) (*57-58*).

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